

Input file Flhl4273new; Output File Flhl4273tra

Sequence length 1743

TCCGGACTAGTTCTAGACCGCTGCGGGCCGCCAGGCGCCGGGA	M	S	P	E	C	A	R	A	A	9
ATG TCC CCT GAA TGC GCG CGG GCA GCG										27
G D A P L R S L E Q A N R T R F P F F S										29
GGC GAC GCG CCC TTG CGC AGC CTG GAG CAA GCC AAC CGC ACC CGC TTT CCC TTC TTC TCC										87
D V K G D H R L V L A A V E T T V L V L										49
GAC GTC AAG GGC GAC CAC CGG CTG GTG CTG GCC GCG GTG GAG ACA ACC GTG CTG GTG CTC										147
I F A V S L L G N V C A L V L V A R R R										69
ATC TTT GCA GTG TCG CTG CTG GGC AAC GTG TGC GCC CTG GTG CTG GTG GCG CGC CGA CGA										207
R R G A T A C L V L N L F C A D L L F I										89
CGC CGC GGC GCG ACT GCC TGC CTG GTA CTC AAC CTC TTC TGC GCG GAC CTG CTC TTC ATC										267
S A I P L V L A V R W T E A W L L G P V										109
AGC GCT ATC CCT CTG GTG CTG GCC GTG CGC TGG ACT GAG GCC TGG CTG CTG GGC CCC GTT										327
A C H L L F Y V M T L S G S V T I L T L										129
GCC TGC CAC CTG CTC TTC TAC GTG ATG ACC CTG AGC GGC AGC GTC ACC ATC CTC ACG CTG										387
A A V S L E R M V C I V H L Q R G V R G										149
GCC GCG GTC AGC CTG GAG CGC ATG GTG TGC ATC GTG CAC CTG CAG CGC GGC GTG CGG GGT										447
P G R R A R A V L L A L I W G Y S A V A										169
CCT GGG CGG CGG GCG CGG GCA GTG CTG CTG GCG CTC ATC TGG GGC TAT TCG GCG GTC GCC										507
A L P L C V F F R V V P Q R L P G A D Q										189
GCT CTG CCT CTC TGC GTC TTC TTT CGA GTC GTC CCG CAA CGG CTC CCC GGC GCC GAC CAG										567
E I S I C T L I W P T I P G E I S W D V										209
GAA ATT TCG ATT TGC ACA CTG ATT TGG CCC ACC ATT CCT GGA GAG ATC TCG TGG GAT GTC										627
S F V T L N F L V P G L V I V I S Y S K										229
TCT TTT GTT ACT TTG AAC TTC TTG GTG CCA GGA CTG GTC ATT GTG ATC AGT TAC TCC AAA										687
I L Q I T K A S R K R L T V S L A Y S E										249
ATT TTA CAG ATC ACA AAG GCA TCA AGG AAG AGG CTC ACG GTA AGC CTG GCC TAC TCG GAG										747
S H Q I R V S Q Q D F R L F R T L F L L										269
AGC CAC CAG ATC CGC GTG TCC CAG CAG GAC TTC CGG CTC TTC CGC ACC CTC TTC CTC CTC										807
M V S F F I M W S P I I I T I L L I L I										289
ATG GTC TCC TTC TTC ATC ATG TGG AGC CCC ATC ATC ATC ACC ATC CTC CTC ATC CTG ATC										867
Q N F K Q D L V I W P S L F F W V V A F										309
CAG AAC TTC AAG CAA GAC CTG GTC ATC TGG CCG TCC CTC TTC TTC TGG GTG GTG GCC TTC										927

FIG 1

T F A N S A L N P I L Y N M T L C R N E 329
ACA TTT GCT AAT TCA GCC CTA AAC CCC ATC CTC TAC AAC ATG ACA CTG TGC AGG AAT GAG 987

W K K I F C C F W F P E K G A I L T D T 349
TGG AAG AAA ATT TTT TGC TGC TTC TGG TTC CCA GAA AAG GGA GCC ATT TTA ACA GAC ACA 1047

S V K R N D L S I I S G * 362
TCT GTC AAA AGA AAT GAC TTG TCG ATT ATT TCT GGC TAA 1086

TTTTTCTTTATAGCCGAGTTTCTCACACCTGGCGAGCTGTGGCATGCTTTTAAACAGAGTTCA^{TT}TCCAGTACCCTCCA

TCAGTGCACCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGCGTCGGTAAATTAAGGGGTGATCACCAA

GTTTCATAATATTTTCCCTTTATAAAAGGATTTGTTGGCCAGGTGCAGTGGTTCATGCCTGTAATCCCAGCAGTTTGGG

AGGCTGAGGTGGGTGGATCACCTGAGGTGAGGAGTTCGAGACCAACCTGACCAACATGGTGAGACCCCGTCTCTACTA

AAAATAAAAAAAAAAATTAGCTGGGAGTGGTGGTGGGCACCTGTAATCCTAGCTACTTGGGAGGCTGAACCAGGAGAAT

CTCTTGAACTGGGAGGCAGAGGTGTCAGTGAGCCGAGATCGTGCCATTGCACTCCAACCAGGGCAACAAGAGTGAAAC

TCCATCTTAAAAAAAAAAAAAAAAAGATTTGTTATGGGTTCCTTTTAAATGTGAAC^{TTTT}TTTACTGTGTTTGTAATATG

ATCAAATTTAATAAATATTTATTTATGACTGTTTCAGCAAAAAAAAAAAAAAAAAAGGGCGG

RTA01/2057957v1

FIG 1 (CONT)

Sequence Description	Score	E-value	N
7tm_1 PF00001 7 transmembrane receptor (rhodopsin)	119.9	4.7e-37	1

Parsed for domains:

Sequence Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
7tm_1	1/1	57	321	..	1	259 {} 119.9 4.7e-37

Alignments of top-scoring domains:

7tm_1: domain 1 of 1, from 57 to 321: score 119.9, E = 4.7e-37

```

*->GNLVilvilrtkkkrtptnifilNLAvADLLflltlppwalyylv
GN+ ++++++r +r +t +LNL ADLLf + p++ ++ --
Flh14273, 57 ONVCALVLVAR-RRRRGATACLVNLFCADLLFISAIPVLAVR-WT 101

gsedWpfgSalCklvtaldvnmYaSillLtaISiDRYLAIvHPlryrrr
e W++G++ C+l+ ++++++ + il+L+a S++R + Iv l+ +r
Flh14273, 102 --EAWLLGPFVACHLLFYVMFLSGSVTILTLAAVSLERMVCIV-HLQRGVR 148

rtspyrAkuvillvwlallslPpLlfswwktveegngtlnvntvCli
+r +v++l+W +++++lP +f+ v + ++ ++ ++ +Cr+
Flh14273, 149 GPGRRARAVLLALIWGYSAVAALPLCVFFRVVPQRLPG--ADQEISICTL 196

dfpeestasvstwlroyvllstlvGFlilvilvcYtrilrtlr.....
+p++++ ++s+ ++ ++ Fl+P lvi++ Y+ Il + + +++++
Flh14273, 197 IWPTIPG-----EISWDVSFVTLNFLVPGLVIVISYSKILQITKsrKr 240

.....kaaktllvvvvFvLCWlPyfivllldtlc
+ + +++++ + +++++ ++ +tl++++v F++ W P i++li +
Flh14273, 241 lcvslayseshgirvsqqdfRLFRFLLMVSFFIMWSPIITILLI IQ 296

.lsiimsstCelervlptallvtlwLayvNscINPiY<-*
++ + + p +++++ + +++++Na+lNPi+Y
Flh14273, 291 nFK-----QDLVIWPSLFFWVVAFTFANSALNPILY 321

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FIG 2

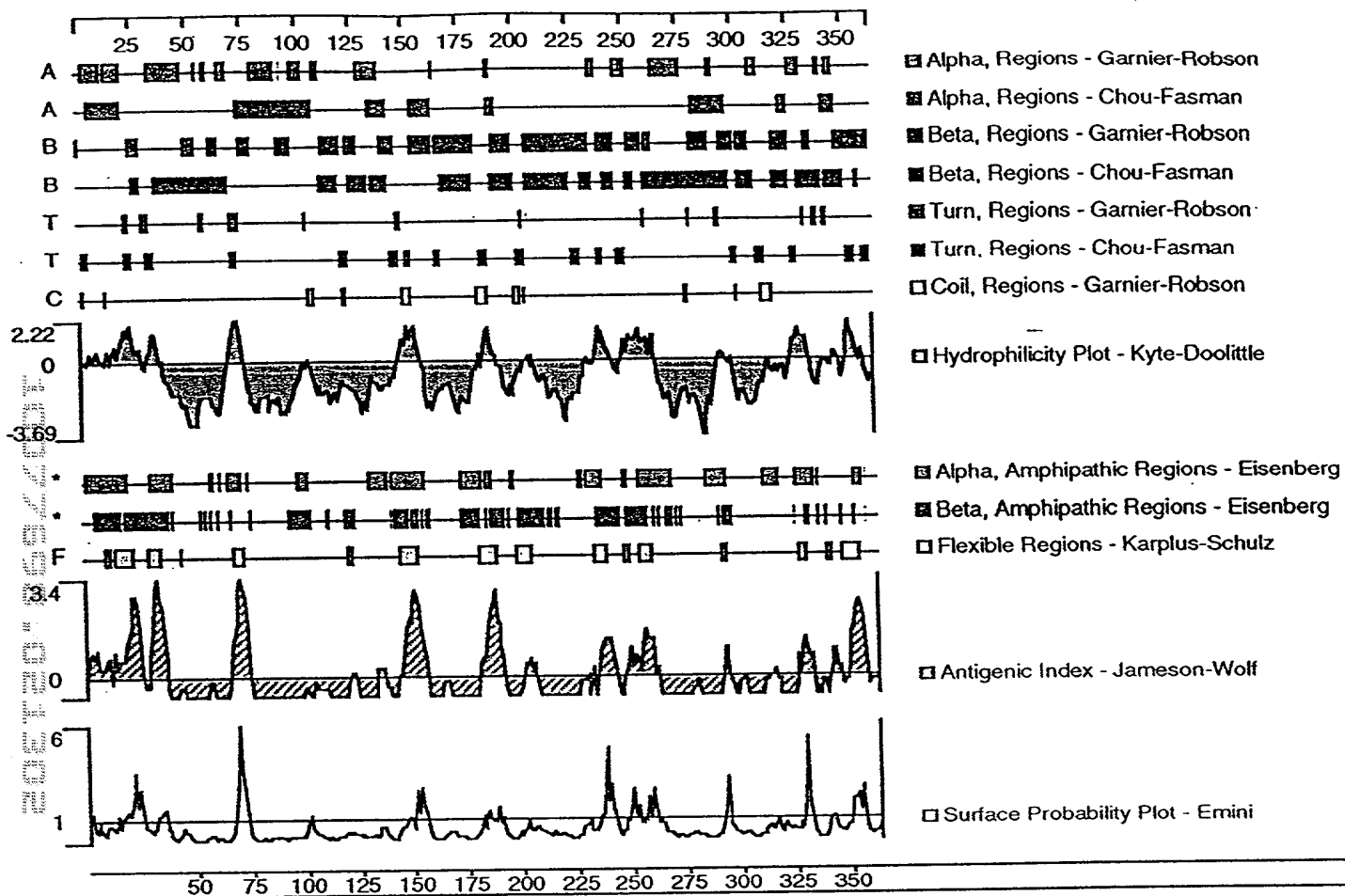


FIG 3

Prosite Pattern Matches for Flh14273,

>PS00001|PDOC00001|ASN_GLYCOSYLATION N-glycosylation site.

Query: 21 NRTR 24

Query: 322 NMTL 325

>PS00004|PDOC00004|CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.

Query: 239 KRLT 242

>PS00005|PDOC00005|PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 237 SRK 239

Query: 350 SVK 352

>PS00006|PDOC00006|CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 256 SQQD 259

>PS00008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 57 GNVCAL 62

Query: 72 CATACL 77

Query: 343 GAILTD 348

>PS00009|PDOC00009|AMIDATION Amidation site.

Query: 150 PGRR 153

>PS00029|PDOC00029|LEUCINE_ZIPPER Leucine zipper pattern.

Query: 106 LGPVACHLLFYVMTLSGVSITL 127

FIG 5

Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
46	66	out->ins	5.1
75	98	ins->out	4.0
113	134	out->ins	4.0
156	177	ins->out	4.9
209	227	out->ins	3.7
266	289	ins->out	6.5
297	321	out->ins	3.2

>Flh14273.

MSPECARAAGDAPLRSLSEQANRTFFPFSQVKGDRHLVLAAVETIVLVLIFAVSLLGNVC
ALVLVARRRRRGATACLVNLFCADLLFISAIPVLAVRWTEAWLLGPFVACHLLFYVMTL
SGSVTILTLAAVSLERMVCIVHLQRCVGRGPGRRARAVLLALIWGYSAVAALPLCVFFRVV
QRLPGADQGEISICTLIWPTIPGEISWDVSVFVTLNFLVPGLVIVISYSKILQITKASRRR
LTVSLAYSESHQIRVSQQDFRLFRFLFLLMVSFIMWSPITITLLILIQNFKQDLVIWP
SLFFWVVAFTFANSALNPILYNMPLCRNEWKKIFCCFWFPEKGAILTDTSVKRNDSLIIIS

Transmembrane segments for presumed mature peptide

Start	End	Orient	Score
14	37	ins->out	4.0
52	73	out->ins	4.0
95	116	ins->out	4.9
148	166	out->ins	3.7
205	228	ins->out	6.5
236	260	out->ins	3.2

>Flh14273._mature

LVLVARRRRRGATACLVNLFCADLLFISAIPVLAVRWTEAWLLGPFVACHLLFYVMTLS
GSVTILTLAAVSLERMVCIVHLQRCVGRGPGRRARAVLLALIWGYSAVAALPLCVFFRVV
QRLPGADQGEISICTLIWPTIPGEISWDVSVFVTLNFLVPGLVIVISYSKILQITKASRRR
LTVSLAYSESHQIRVSQQDFRLFRFLFLLMVSFIMWSPITITLLILIQNFKQDLVIWPS
LFFWVVAFTFANSALNPILYNMPLCRNEWKKIFCCFWFPEKGAILTDTSVKRNDSLIIISG

FIG 6

Input file 14273m; Output File 14273mtra
Sequence length 1560

TTGCCAAGCTCAGCGTAAGCCTCTTCCACTGCAATCTCACAGAAGGGGTTCATGGAGTGTTCACACCATCAGTGACCA

CTCCAGACTTGTCCGGCTTTACCGAATCTTCACAGCGGAGTCGATGACCCTCTTGACAGCCACGAGCGCGCGCAGCTC

	M	S	P	E	C	A	Q	T	T	G	10									
CGCCATCTTCCCGACGCGTGGGCGGGCGCCCGGC	ATG	TCC	CCT	GAG	TGT	GCA	CAG	ACG	ACG	GGC	30									
P	G	P	S	H	T	L	D	Q	V	N	R	T	H	F	P	F	F	S	D	30
CCT	GGT	CCC	TCG	CAC	ACC	CTG	GAC	CAA	GTC	AAT	CGC	ACC	CAC	TTC	CCT	TTC	TTC	TCG	GAT	90
V	K	G	D	H	R	L	V	L	S	V	V	E	T	T	V	L	G	L	I	50
GTC	AAG	GGC	GAC	CAC	CGG	TTG	GTG	TTG	AGC	GTC	GTG	GAG	ACC	ACC	GTT	CTG	GGA	CTC	ATC	150
F	V	V	S	L	L	G	N	V	C	A	L	V	L	V	A	R	R	R	R	70
TTT	GTC	GTC	TCA	CTG	CTG	GGC	AAC	GTG	TGT	GCT	CTA	GTG	CTG	GTG	GCG	CGC	CGT	CGG	CGC	210
R	G	A	S	A	S	L	V	L	N	L	F	C	A	D	L	L	F	T	S	90
CGT	GGG	GCG	TCA	GCC	AGC	CTG	GTG	CTC	AAC	CTC	TTC	TGC	GCG	GAT	TTG	CTC	TTC	ACC	AGC	270
A	I	P	L	V	L	V	V	R	W	T	E	A	W	L	L	G	P	V	V	110
GCC	ATC	CCT	CTA	GTG	CTC	GTC	GTG	CGC	TGG	ACT	GAG	GCC	TGG	CTG	TTG	GGG	CCC	GTC	GTC	330
C	H	L	L	F	Y	V	M	T	M	S	G	S	V	T	I	L	T	L	A	130
TGC	CAC	CTG	CTC	TTC	TAC	GTG	ATG	ACA	ATG	AGC	GGC	AGC	GTC	ACG	ATC	CTC	ACA	CTG	GCC	390
A	V	S	L	E	R	M	V	C	I	V	R	L	R	R	G	L	S	G	P	150
GCG	GTC	AGC	CTG	GAG	CGC	ATG	GTG	TGC	ATC	GTG	CGC	CTC	CGG	CGC	GGC	TTG	AGC	GGC	CCG	450
G	R	R	T	Q	A	A	L	L	A	F	I	W	G	Y	S	A	L	A	A	170
GGG	CGG	CGG	ACT	CAG	GCG	GCA	CTG	CTG	GCT	TTC	ATA	TGG	GGT	TAC	TCG	GCG	CTC	GCC	GCG	510
L	P	L	Y	I	L	F	R	V	V	P	Q	R	L	P	G	G	D	Q	E	190
CTG	CCC	CTC	TAC	ATC	TTG	TTC	CGC	GTG	GTC	CCG	CAG	CGC	CTT	CCC	GGC	GGG	GAC	CAG	GAA	570
I	P	I	C	T	L	D	W	P	N	R	I	G	E	I	S	W	D	V	F	210
ATT	CCG	ATT	TGC	ACA	TTG	GAT	TGG	CCC	AAC	CGC	ATA	GGA	GAA	ATC	TCA	TGG	GAT	GTG	TTT	630
F	E	T	L	N	F	L	V	P	G	L	V	I	V	I	S	Y	S	K	I	230
TTT	GAG	ACT	TTG	AAC	TTC	CTG	GTG	CCG	GGA	CTG	GTC	ATT	GTG	ATC	AGT	TAC	TCC	AAA	ATT	690
L	Q	I	T	K	A	S	R	K	R	L	T	L	S	L	A	Y	S	E	S	250
TTA	CAG	ATC	ACG	AAA	GCA	TCG	CGG	AAG	AGG	CTT	ACG	CTG	AGC	TTG	GCA	TAC	TCT	GAG	AGC	750
H	Q	I	R	V	S	Q	Q	D	Y	R	L	F	R	T	L	F	L	L	M	270
CAC	CAG	ATC	CGA	GTG	TCC	CAA	CAA	GAC	TAC	CGA	CTC	TTC	CGC	ACG	CTC	TTC	CTG	CTC	ATG	810
V	S	F	F	I	M	W	S	P	I	I	I	T	I	L	L	I	L	I	Q	290
GTT	TCC	TTC	TTC	ATC	ATG	TGG	AGT	CCC	ATC	ATC	ATC	ACC	ATC	CTC	CTC	ATC	TTG	ATC	CAA	870
N	F	R	Q	D	L	V	I	W	P	S	L	F	F	W	V	V	A	F	T	310
AAC	TTC	CGG	CAG	GAC	CTG	GTC	ATC	TGG	CCA	TCC	CTT	TTC	TTC	TGG	GTG	GTG	GCC	TTC	ACG	930
F	A	N	S	A	L	N	P	I	L	Y	N	M	S	L	F	R	N	E	W	330
TTT	GCC	AAC	TCT	GCC	CTA	AAC	CCC	ATA	CTG	TAC	AAC	ATG	TCG	CTG	TTC	AGG	AAC	GAA	TGG	990
R	K	I	F	C	C	F	F	F	P	E	K	G	A	I	F	T	D	T	S	350
AGG	AAG	ATT	TTT	TGC	TGC	TTC	TTT	TTT	CCA	GAG	AAG	GGA	GCC	ATT	TTT	ACA	GAT	ACG	TCT	1050
V	R	R	N	D	L	S	V	I	S	S	*									362
GTC	AGG	CGA	AAT	GAC	TTG	TCT	GTT	ATT	TCC	AGC	TAA									1085

CTAGCCTCTGGTGCCAGGTGAACACGGGTGTCATGTAAAGGGAGTTAACTTCAAGGAAAGCCACCAAGTGCSCCCTGC

Year	Area	Population	Area	Population	Area	Population
1970	100	100	100	100	100	100
1971	100	100	100	100	100	100
1972	100	100	100	100	100	100
1973	100	100	100	100	100	100
1974	100	100	100	100	100	100
1975	100	100	100	100	100	100
1976	100	100	100	100	100	100
1977	100	100	100	100	100	100
1978	100	100	100	100	100	100
1979	100	100	100	100	100	100
1980	100	100	100	100	100	100
1981	100	100	100	100	100	100
1982	100	100	100	100	100	100
1983	100	100	100	100	100	100
1984	100	100	100	100	100	100
1985	100	100	100	100	100	100
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1994	100	100	100	100	100	100
1995	100	100	100	100	100	100
1996	100	100	100	100	100	100
1997	100	100	100	100	100	100
1998	100	100	100	100	100	100
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2001	100	100	100	100	100	100
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2004	100	100	100	100	100	100
2005	100	100	100	100	100	100
2006	100	100	100	100	100	100
2007	100	100	100	100	100	100
2008	100	100	100	100	100	100
2009	100	100	100	100	100	100
2010	100	100	100	100	100	100
2011	100	100	100	100	100	100
2012	100	100	100	100	100	100
2013	100	100	100	100	100	100
2014	100	100	100	100	100	100
2015	100	100	100	100	100	100
2016	100	100	100	100	100	100
2017	100	100	100	100	100	100
2018	100	100	100	100	100	100
2019	100	100	100	100	100	100
2020	100	100	100	100	100	100

Query: 14273m,

Scores for sequence family classification (score includes all domains):

Sequence	Description	Score	E-value	N
7tm_1	PF00001 7 transmembrane receptor (rhodopsin	118.8	1e-35	1

Parsed for domains:

Sequence	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
7tm_1	1/1	57	321	1	259	118.8	1e-36

Alignments of top-scoring domains:

7tm_1: domain 1 of 1, from 57 to 321: score 118.8, E = 1e-36

```

*->GNILVilvilrtkkrlrtptnifilNLAVADLLflltlppwalyylvg
14273m. 57 GN+ ++++++R +++R ++ ++LNL ADLLf+ + p++ ++ ++
GNVCALVLVAR-RRERGASASLVNLFCADLLFTSAIPVLVVR-WT 101

gsadWpfGsalCKlvtaldvnmmyaSilLLtAISiDRYIAIvhPlryrry
14273m. 102 e W++G+++C+l+ ++++++ + il+L+a S++R + IV L= +
--EAWLLGFPVVCHLLFPYVMTKSGSVTILTLAAVSLERMVCIV-RLRRGLS 148

rtsprxA.kvvillvWvlalllsIPllfswvktveegngtlnvntvC1
14273m. 149 YR+++++++W ++l++lP ++++ v + ++g ++ +C+
GP-GRRTQAALLAFIWGYSAALPLYILFRVVPQRLPGGD--QEIPICT 195

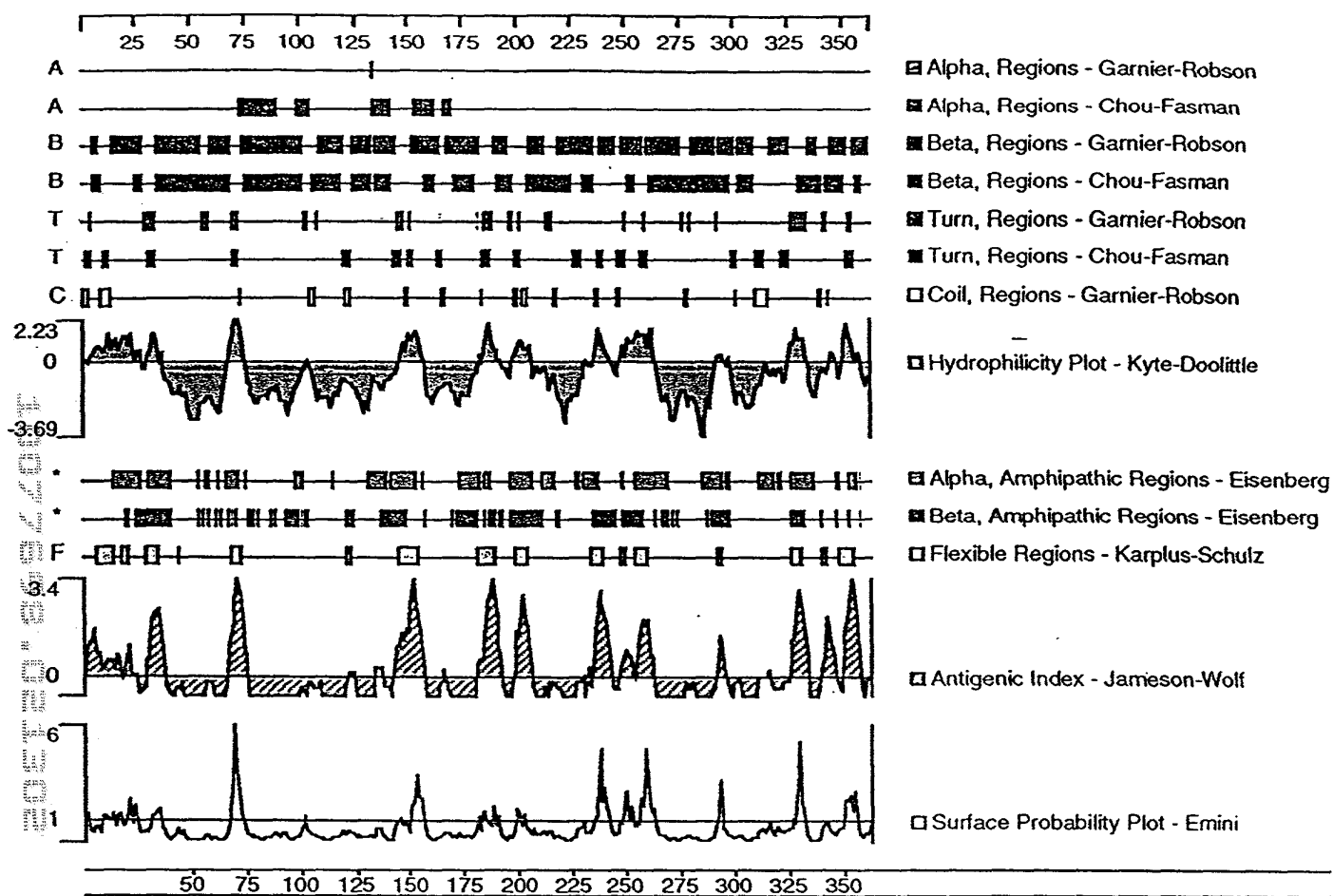
idfpeestasvstwlrsyvlstlvGFllPllvilvcYtrIlrtlr....
14273m. 196 +d+p-+ + ++S+ +++ ++ Fl+P lv++ Y+ Il + + +++
LDWPNRIG-----EISWDVFPETLNFLVPGLVVISYSKILQITKsrk 239

.....kaaktllvvvvFv1CWlPyfivllldt1
14273m. 240 + + + +++++ + ++++ ++ +tl++++v F++ W P i++ll +
rltlalayseshqirvsqqdyRLFRTLFLLMVSFFIMWSPIIITILLILI 289

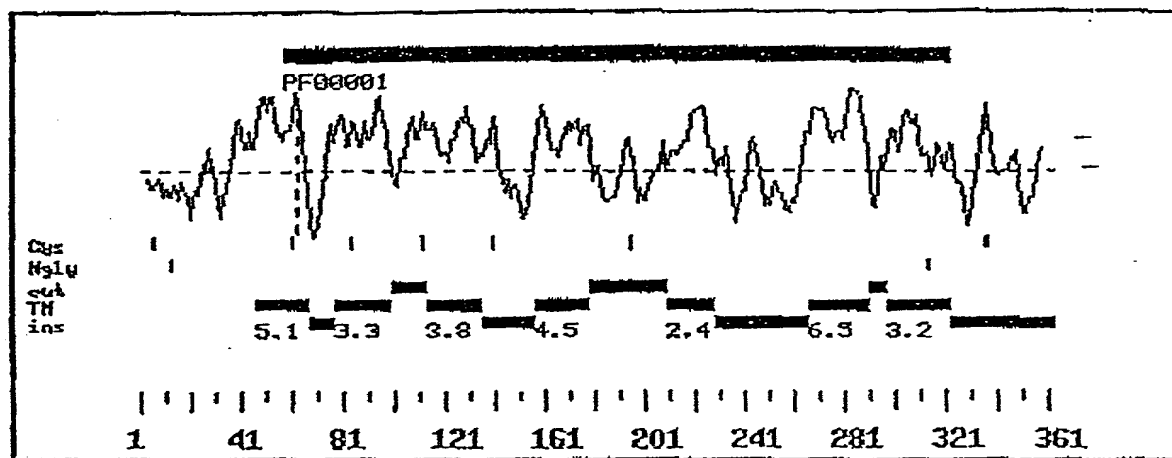
c.lsiimsstCelervlptallvtilwlayvNsc1NPiIY<-*
14273m. 290 ++ + + p ++++ + +++++Ns+1NPi+Y
QnFR-----QDLVIWPSLFFWVVAFTFANSALNPILY 321

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FIG 8



Analysis of 14273m, (362 aa)



>14273m, 1086 bases, 6943 checksum.

MSPECAQTTGPGPSHTLDQVNRTHFPFFSDVKGDRVLVSVVETTVLGLIFVVSLLGNVC
 ALVLVARRRRRGASASLVNLNFCADLLFTSAIPLVLVVRWTEAWLLGPVVCHLLFYVMTM
 SGSVTILTLAAVSLERMVCIVRLRRGLSGPGRRTQAALLAFIWGYSALAALPLYILFRVV
 PQRLPGGDQEIPICITLDWPNRIGEISWDVFFETLNFVLPGLVIVISYSKILQITKASRR
 LTLSLAYSESHQIRVSQQDYRLFRTLFLLMVSFFIMWSPITITILLILQNFRODLVIWP
 SLFFWVVAFTFANSALNPILYNMSLFRNEWKIFCCFFPEKGAIFTDTSVRNDLSVIS
 S*

FIG 10

Prosite Pattern Matches for 14273m,

>PS00001|PDOC00001|ASN_GLYCOSYLATION N-glycosylation site.

Query: 21 NRTI 24

Query: 322 NMSL 325

>PS00002|PDOC00002|GLYCOSAMINOGLYCAN Glycosaminoglycan attachment site.

RU Additional rules:

RU There must be at least two acidic amino acids (Glu or Asp) from -2 to

RU -4 relative to the serine.

Query: 148 SGPG 151

>PS00004|PDOC00004|CAMP_PHOSPHO_SITE CAMP- and cGMP-dependent protein kinase phosphorylation

Query: 239 KRLT 242

>PS00005|PDOC00005|PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 237 SRX 239

Query: 350 SVR 352

>PS00006|PDOC00006|CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 40 SVVE 43

Query: 256 SQOD 259

>PS00008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 57 GNVCL 62

Query: 72 GASASL 77

Query: 343 GAIFTD 348

>PS00009|PDOC00009|AMIDATION Amidation site.

Query: 150 PGRR 153

Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
46	66	out->ins	5.1
77	98	ins->out	3.3
113	134	out->ins	3.8
156	177	ins->out	4.5
209	227	out->ins	2.4
266	289	ins->out	6.5
297	321	out->ins	3.2

>14273m,
MSPECAQTTGPGPSHTLDQVNRTHFPFFSDVKGDHRLVLSVVETTTLGLIFVVSLLGNVC
ALVLVARRRRRGASASLVNLFCADLLFTSAIPLVLVVRWTEAWLLGPVVCHLLFYVMTM
SGSVTILTLAAVSLERMVCIVRLRRLSGPGRRTQAALLAFIWCYSALAALPLYILFRVV
PQRLPGGDQEIPICTLDWPNRIGEISWDVFFETLNLVPLVTVISYSKILQITKASRKR
LTLSLAYSESHQIRVSQQDYRLFTLFLLMVSFFIMWSPITITILLILIQNFRQDLVIWP
SLFPWVVAFTFANSALNPILYNMSLFRNEWKIFCCFFFPKGAIFTDTSVRRNDLSVIS
S

Transmembrane segments for presumed mature peptide

Start	End	Orient	Score
16	37	ins->out	3.3
52	73	out->ins	3.8
95	116	ins->out	4.5
148	166	out->ins	2.4
205	228	ins->out	6.5
236	260	out->ins	3.2

>14273m, _mature
LVLVARRRRRGASASLVNLFCADLLFTSAIPLVLVVRWTEAWLLGPVVCHLLFYVMTM
GSVTILTLAAVSLERMVCIVRLRRLSGPGRRTQAALLAFIWCYSALAALPLYILFRVV
PQRLPGGDQEIPICTLDWPNRIGEISWDVFFETLNLVPLVTVISYSKILQITKASRKR
LTLSLAYSESHQIRVSQQDYRLFTLFLLMVSFFIMWSPITITILLILIQNFRQDLVIWP
SLFPWVVAFTFANSALNPILYNMSLFRNEWKIFCCFFFPKGAIFTDTSVRRNDLSVIS